

# GENETIC MONITORING AND EVALUATION OF SNAKE RIVER SALMON AND STEELHEAD

8909600

## SHORT DESCRIPTION:

Evaluate the genetic consequences of using hatchery fish to supplement natural populations of chinook salmon and steelhead in the Snake River Basin.

## SPONSOR/CONTRACTOR: NMFS

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## SUB-CONTRACTORS:

In past years, we have contracted with Mr. Chuck Peven, Chelan County PUD, to age juvenile steelhead by reading otoliths collected in this study. We may do so again this year. Cost is approximately \$1,500-2,000 per year.

## GOALS

### GENERAL:

Maintains biological diversity, Maintains genetic integrity

### ANADROMOUS FISH:

Research, M&E

### NPPC PROGRAM MEASURE:

7.2; 7.3B.2; 7.4D.2; 7.4L.1

### BIOLOGICAL OPINION ID:

Conservation Recommendation #3 from the "Biological Opinion for 1995 to 1998 Hatchery Operations in the Columbia River Basin" (April 5, 1995) stipulates that "The action agencies should conduct monitoring and evaluation studies for hatchery programs. This should assist NMFS in evaluating the effects of hatchery programs on listed and unlisted natural fish."

### OTHER PLANNING DOCUMENTS:

Proposed Recovery Plan for Snake River Salmon: Tasks 4.1b (Priority 1), 4.3a (Priority 1).

<u>TARGET STOCK</u>	<u>LIFE STAGE</u>	<u>MGMT CODE (see below)</u>
Minam R. spring chinook	Juvenile	N,(L)
Valley Cr. spr/sum chinook	Juvenile	N,(L)
Sawtooth Hatchery spring chinook	Juvenile	A,S,(L),W
Marsh Cr. spring chinook	Juvenile	N,(L)
McCall Hatchery summer chinook	Juvenile	A,S,(L),W
Johnson Cr. Summer chinook	Juvenile	S,(L)
Secesh R. summer chinook	Juvenile	N,(L)
South Fork summer chinook	Juvenile	S,(L)
Imnaha R. spr/sum chinook	Juvenile	S,(L)
Imnaha Hatchery spr/sum. Chinook	Juvenile	A,S,(L),W
Lookingglass Hatchery spring chinook	Juvenile	A
Upper Salmon R. spr/sum chinook	Juvenile	S,(L)
Wenaha R. spring chinook	Juvenile	N,(L)
Chesnimnus Cr. Steelhead	Juvenile	S,(P)
Grande Ronde R. spring chinook	Juvenile	S,(L)
Catherine Cr. Spring chinook	Juvenile	S,(L)

U. Tucannon R. steelhead	Juvenile	N,(P)
L. Tucannon R. steelhead	Juvenile	S,(P)
Tucannon Hatchery steelhead	Juvenile	A,S,W
Lochsa R. steelhead	Juvenile	S,(P)
Selway R. steelhead	Juvenile	N,(P)
Dworshak Hatchery steelhead	Juvenile	A,S,W
Wallowa Hatchery steelhead	Juvenile	A,S,W
Deer Cr. Steelhead	Juvenile	S,(P)
Lick Cr. Steelhead	Juvenile	N,(P)
L. Sheep Cr. Hatchery steelhead	Juvenile	A,S,W
L. Sheep Cr. Steelhead	Juvenile	S,(P)
Lostine R. spring chinook	Juvenile	S,(L)

#### **AFFECTED STOCK**

No other species likely to be affected by this study

#### **BENEFIT OR DETRIMENT**

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## **BACKGROUND**

### **STREAM AREA AFFECTED**

#### **Stream name:**

Includes many streams; see target stocks section

#### **Stream miles affected:**

many

#### **Hydro project mitigated:**

Not applicable to this study.

#### **Project is an office site only**

### **LAND AREA INFORMATION**

#### **Subbasin:**

Includes many sub-basins; see target stocks section

#### **Land ownership:**

both

#### **Acres affected:**

many

#### **Habitat types:**

Not applicable to this study.

### **HISTORY:**

The study began in fall of 1989, and analysis is currently underway for samples from the 7th year of field collections. The basic research plan involves eight different supplementation programs (four each for chinook salmon and steelhead). The experimental design calls for yearly samples from hatchery stocks used in outplanting, from a natural population affected by releases from that hatchery, and from a wild population in the same drainage not intended to be affected. Although the central focus of the research has remained unchanged, the sampling design has been somewhat flexible to respond to high priority issues associated with supplementation in the Snake River basin that have arisen since 1989. For example, for the past several years we have conducted intensive genetic monitoring in the Grande Ronde Basin to assess impacts to natural populations of straying by Rapid River stock hatchery fish. The initial study design identified the Lostine River as the only natural/wild population to be sampled in the Grande Ronde Basin.

### **BIOLOGICAL RESULTS ACHIEVED:**

This study involves monitoring, evaluation, and research and thus does not directly produce fish or alter habitat. However, because supplementation is viewed as a central component of the Fish and Wildlife Program to restore salmon and steelhead in the Columbia River Basin, and also plays a significant role in the proposed Recovery Plan for Snake River Salmon, information (such as is derived from this study) that helps determine the most effective ways of supplementing natural populations will lead directly to enhancement of the resource.

### **PROJECT REPORTS AND PAPERS:**

Waples, R. S., D. J. Teel, and P. B. Aebersold. 1991. A genetic monitoring and evaluation program for supplemented populations of salmon and steelhead in the Snake River Basin. Annual Report of Research to Bonneville Power Administration, Portland, OR, 50p.

Waples, R. S., O. W. Johnson, P. B. Aebersold, C. K. Shiflett, D. M. VanDoornik, D. J. Teel, and A. E. Cook. 1993. A genetic monitoring and evaluation program for supplemented populations of salmon and steelhead in the Snake River Basin. Annual

Report of Research to Bonneville Power Administration, Portland, OR, 179 p.

Utter, F. M., R. S. Waples, and D. J. Teel. 1992. Genetic isolation of previously indistinguishable chinook salmon populations of the Snake and Klamath Rivers: Limitations of negative data. *Fish. Bull. (U.S.)* 90:770-777.

Park, L. K., P. Moran, and R. S. Waples (editors). 1994. Application of DNA technology to the management of Pacific salmon. Proceedings of the workshop, 22-23 March 1993, Seattle, WA. U.S. Dept. Commerce, NOAA Tech. Memo. NMFS-NWFSC-17, 178 p.

Waples, R. S., and C. Do. 1994. Genetic risk associated with supplementation of Pacific salmonids: Captive broodstock programs. *Can. J. Fish. Aquat. Sci.* 51 (Suppl. 1):310-329.

Park, L. K., AND P. Moran. 1994. Developments in molecular genetic techniques in fisheries. *Reviews in Fish and Fisheries Biology* 4:272-299.

Park, L. K., P. Moran, AND D. Dightman. 1995. A polymorphism in intron D of the chinook salmon growth hormone 2 gene. *Animal Genetics*. 2(26):285.

Park, L. K., P. Moran, and D. Nickerson. 1994. Application of the oligonucleotide ligation assay (OLA) to the study of chinook salmon populations from the Snake River. In, L. K. Park, P. Moran and R. S. Waples (eds.). Application of DNA technology to the management of Pacific salmon. U.S. Dep. Commer., NOAA Tech. Memo NMFS NWFSC-17:91-97.

Park, L. K., P. Moran AND D. A. Dightman. 1996. A chinook salmon PCR RFLP marker in the p53 locus. *Animal Genetics* 27:127-128.

#### **ADAPTIVE MANAGEMENT IMPLICATIONS:**

As discussed under "Biological need," a comprehensive monitoring and evaluation program (including but not limited to genetics) is essential for an adaptive management approach to supplementation. Results from this study can also be (and have been) used to address common, practical management questions such as, How similar genetically are the hatchery stock and the targeted natural population(s), and how does this relationship change over time? Is there fine-scale stock structure that may be at risk from certain broodstock collection or release strategies? Are there indications that supplementation is genetically impacting wild populations that were not intended to be affected? Is there evidence for erosion of genetic diversity in hatchery and/or natural populations? What genetic characteristics are found in supplementation programs that are "successful" (as measured by stock production, productivity, or other measures), and what are found in programs that are less successful? Examples of the use of information from this study in an adaptive management context include 1) the Snake River Salmon Recovery Team, based in part on results from early years of this study, identified 35-40 local sub-populations of spring/summer chinook salmon that should be managed separately for recovery; 2) Results from this study played a key role in the 1996 Scientific Panel's evaluation of the federal/state vs tribal dispute over the role of supplementation in the Grande Ronde Basin.

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## **PURPOSE AND METHODS**

#### **SPECIFIC MEASUREABLE OBJECTIVES:**

- \* Quantify genetic differences/similarities between hatchery and wild/natural populations and how this pattern changes over time.
- \* Quantify changes over time in levels of genetic variability within populations.
- \* Estimate effective population size and the ratio  $N_e/N$  for each population each year.
- \* Use genetic data to estimate natural levels of gene flow among geographic sub-populations, which can be compared with levels associated with supplementation.

#### **CRITICAL UNCERTAINTIES:**

The major uncertainty for this project is the continued availability of samples from the natural populations. Comprehensive data for allozyme analyses requires sacrificing fish. As noted above, our sampling strategy for chinook salmon was modified in 1995 and 1996 to avoid lethal sampling. Non-lethal DNA sampling, however, is not expected to be affected by these concerns. Availability of allozyme samples from natural populations depends primarily on the abundance of adults the previous year (or previous 1-3 years for steelhead). 1996 was a better return year for chinook salmon than 1994 and 1995, and strong returns are expected in 1997 and 1998, so we expect to resume allozyme sampling this year or next year. Appropriate levels of sampling will be determined in consultation with state agency biologists, and through the process of securing state and federal ESA collection permits.

It is not expected that this study will entail any risks to other stocks.

#### **BIOLOGICAL NEED:**

The central tenet of adaptive management is maintaining flexibility to respond to biological indicators of the success or failure of s

pecific management strategies. This flexibility, however, is of little use without an adequate monitoring and evaluation program to provide the basis for making scientifically-based decisions. Supplementation is an experimental strategy that has considerable promise but also many associated uncertainties. The genetic consequences of supplementing natural populations with hatchery reared fish are among the biggest uncertainties, and this issue cannot be addressed without a monitoring program that focuses on genetic markers. This study is thus an essential component of a more comprehensive, cross-disciplinary monitoring and evaluation program for salmon supplementation.

#### **HYPOTHESIS TO BE TESTED:**

This study directly addresses a number of testable hypotheses:

- \* There are no genetic differences among natural populations, except those that can be attributed to sampling error and random year-to-year variation. (Alternative hypothesis: differences exist between geographic populations).
- \* There are no genetic differences between hatchery populations and natural populations they were derived from. (Alternative hypothesis: differences exist between hatchery and natural populations).
- \* Populations that have been supplemented show the same magnitude of genetic change over time as unsupplemented populations. (Alternative hypothesis: supplemented populations show greater differences).
- \* Populations in which genetic effects of supplementation can be detected show the same patterns of abundance and productivity as unsupplemented populations [requires collating results with data from other projects]. (Alternative hypotheses: supplemented populations show greater or less productivity).
- \* Non-target wild populations have not been genetically affected by hatchery strays. (Alternative hypothesis: genetic changes are detectable in non-target stocks.)
- \* The relationship between effective population size ( $N_e$ ) and total population size ( $N$ ) is the same in hatchery and natural populations. (Alternative hypotheses: ratio  $N_e/N$  is higher or lower in hatchery populations).
- \* The relationship between  $N_e$  and  $N$  in natural populations is the same in years of high and low escapements. (Alternative hypothesis: ratio  $N_e/N$  differs with abundance.)
- \* Inter-locus variance of  $F$  (a measure of allele frequency change over time) is no larger than would be expected if all changes are due to sampling error and genetic drift. (Alternative hypothesis: interlocus variance is higher than expected, suggesting some loci may be under selection.)
- \* Current natural populations in the Grande Ronde basin are not more similar to the Rapid River stock from Lookingglass Hatchery than they were historically. [Based on DNA analysis of archived scales.] (Alternative hypothesis: the populations are more similar to Rapid River stock than they were historically).

#### **ALTERNATIVE APPROACHES:**

We have not rejected any approaches that might accomplish the program goals. As described under section A above, we have modified the experimental design to accommodate concerns for sacrificing juvenile fish following record low adult returns in 1994 and 1995.

#### **JUSTIFICATION FOR PLANNING:**

Not applicable to this study

#### **METHODS:**

In each basin for each species, the experimental design calls for samples of juveniles from hatchery populations used in supplementation, natural populations targeted for supplementation, and non-target wild populations. Most populations are sampled every year or every other year. Sample collection is coordinated with local state and tribal fishery biologists. Samples are analyzed using protein electrophoresis for over 35 variable gene loci in chinook salmon and over 50 variable loci in steelhead. A subset of the fish in each sample are also examined for a suite of mitochondrial and nuclear DNA markers. DNA data may be taken from fin clips and archived scales as well as whole fish. Other biological information taken from the fish includes length and age for steelhead.

A variety of standard statistical analyses are performed on the data, including indices of genetic variability, tests of conformance to Hardy-Weinberg genotypic proportions, contingency chi-square tests, genetic distance, F-statistics, and hierarchical gene diversity analysis. In addition, statistical approaches developed at the NMFS' Northwest Fisheries Science Center specifically for use with Pacific salmon are used to analyze data for duplicated gene loci and for estimating effective population size using both temporal changes in allele frequency and gametic disequilibrium.

For samples analyzed during fiscal years 1989-95, samples of 60-100 juveniles per population were collected as fry or parr in late summer or early fall. Because of record low returns of chinook salmon to the Snake River in 1994 and 1995, parr collections

in 1995 and 1996 (for analysis in FY1996 and FY1997) were modified to avoid sacrificing any individuals. Instead, fin clips for DNA analysis were taken from fish already being collected for other purposes (e.g., PIT-tagging or smolt monitoring).

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## PLANNED ACTIVITIES

### SCHEDULE:

<u>Planning Phase</u>	<u>Start</u> FY1989	<u>End</u> FY1989	<u>Subcontractor</u>
<b>Task</b> Activities in FY97 will proceed as outlined above, and we will continue to monitor both steelhead and chinook salmon populations to determined appropriate levels of sampling. We expect to restrict sampling of chinook salmon in 1996 to non-lethal fin clips for DNA analysis, as described above. In FY1998 we hope to resume samples for allozyme analysis if runs return to more abundant levels. The study was initially designed to run for at least 10 years, so FY2000 will be a time for review and evaluation of results obtained through that time.			

### PROJECT COMPLETION DATE:

1999

### CONSTRAINTS OR FACTORS THAT MAY CAUSE SCHEDULE OR BUDGET CHANGES:

The only significant source of risk from this study is depletion of the natural population from sampling. In "normal" return years, the level of take is a tiny fraction of the parr population. In years of critically low returns, sampling is a more serious concern, and this risk has been dealt with as described above.

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## OUTCOMES, MONITORING AND EVALUATION

### SUMMARY OF EXPECTED OUTCOMES

#### Expected performance of target population or quality change in land area affected:

We expect the results from this study to provide the following types of information:

- \* Population genetic structure of chinook salmon and steelhead in the Snake River Basin.
- \* Effectiveness of supplementation as measured by genetic impacts on target natural populations and non-target wild populations.
- \* A better understanding of the relationship between effective and total population size in natural and hatchery populations.
- \* A better understanding of the strengths and weaknesses of using allozymes to monitor salmon and steelhead supplementation.
- \* An evaluation of the advantages and disadvantages of using DNA markers for monitoring and evaluation of salmon supplementation.

#### Present utilization and conservation potential of target population or area:

The target populations of chinook salmon have not supported direct, non-tribal harvest for over 20 years. This study includes many of the core populations for both the Snake River steelhead and spring/summer chinook salmon ESUs, so collectively they represent substantial conservation potential.

#### Assumed historic status of utilization and conservation potential:

Historically, populations of chinook salmon were much more abundant and supported substantial tribal and non-tribal fisheries.

#### Long term expected utilization and conservation potential for target population or habitat:

The long-term goal is to restore sustainable natural populations that can support harvest. Supplementation may be a temporary or permanent part of this picture.

#### Contribution toward long-term goal:

This study provides information about how best to integrate natural and hatchery production in a sustainable way.

#### Indirect biological or environmental changes:

This study should not result directly in any environmental changes. Improved information for use in fishery management should result in biological changes with a positive effect on target populations.

**Physical products:**

On a yearly basis, this study provides genetic information for a suite of 60-70 allozyme loci and 10 or more DNA markers for samples from a number of spring/summer chinook salmon and steelhead populations.

**Environmental attributes affected by the project:**

This project is not expected to have any direct effect on environmental attributes.

**Changes assumed or expected for affected environmental attributes:**

Not applicable to this study.

**Measure of attribute changes:**

Not applicable to this study.

**Assessment of effects on project outcomes of critical uncertainty:**

See response to item A under "SCIENTIFIC BASIS OR RATIONALE FOR PROJECT," above.

**Information products:**

•By the end of the current project period, we will have performed genetic analysis of over 12,000 chinook salmon and steelhead, and meristic analysis has been completed for several thousand fish. See Section 2 for a list of reports and papers that have resulted from this study. Results of this study have been used in a number of fishery management decisions in the basin. Genetic information developed during this project was used in the ESA listing determination for Snake River spring/summer chinook salmon and in the ESA status review for west coast steelhead. Genetic information has also been provided to several agencies and groups interested in supplementation in the Snake River Basin, including ODFW, IDFG, WDFW, the Nez Perce and Umatilla tribes, and the Snake River Salmon Recovery Team. Results from this study played a key role in the 1996 Scientific Panel's evaluation of the federal/state vs tribal dispute over the role of supplementation in the Grande Ronde Basin. In March 1993, in part using funds provided by BPA through this project, NMFS hosted an international DNA workshop in Seattle that addressed both technical and management issues. Proceedings of the workshop were published by NMFS in 1994. Funding from this project also enabled us to carry out computer modeling of the genetic consequences of using captive broodstocks to supplement natural populations. Results of that research have been published in the Canadian Journal of Fisheries and Aquatic Sciences.

**Coordination outcomes:**

Study sites and ample collection are coordinated with local state and tribal fishery biologists on an ongoing basis. In addition to formal reports, preliminary information from this study is communicated regularly to affected agencies to help in their management decisions. Our study also uses a number of types of biological information produced by other studies (e.g, redd or weir counts to obtain an estimate of population size, age structure and sex ratio of the populations, etc.).

**MONITORING APPROACH**

**Provisions to monitor population status or habitat quality:**

This study is a monitoring study.

**Data analysis and evaluation:**

A variety of standard statistical analyses are performed on the data, including indices of genetic variability, tests of conformance to Hardy-Weinberg genotypic proportions, contingency chi-square tests, genetic distance, F-statistics, and hierarchical gene diversity analysis. In addition, statistical approaches developed at the Northwest Fisheries Science Center specifically for use with Pacific salmon are used to analyze data for duplicated gene loci and for estimating effective population size using both temporal changes in allele frequency and gametic disequilibrium.

### Information feed back to management decisions:

See also item L above. In addition to formal reports, papers, and other documents, we regularly discuss preliminary results with fishery managers who have to make real time decisions about how to manage supplementation programs.

### Critical uncertainties affecting project's outcomes:

See response to item A under "SCIENTIFIC BASIS OR RATIONALE FOR PROJECT," above. Results from a genetic monitoring study are most useful if they can be interpreted in the context of other biological and demographic information for the populations in question. A number of separately funded projects in Oregon, Idaho, and Washington are gathering useful information such as redd counts, age structure, sex ratio, adult size, fecundity, productivity, stage specific survivals, and other life history traits.

## EVALUATION

Some indicators of project success:

- \* Quantity and quality of genetic data produced
- \* Responsiveness and flexibility to modify experimental design to accommodate management needs, without sacrificing scientific rigor.
- \* Successful development of DNA markers for retrospective genetic analyses using archived scales.
- \* Use of results from this study in regional fishery management decisions (e.g., ESA recovery planning; ESA permitting process; identification of conservation units; management of straying by production hatcheries; choice of broodstock for supplementation).

### Incorporating new information regarding uncertainties:

The major uncertainty in recent years--availability of allozyme samples due to reduced run size--will be dealt with on a yearly basis, based on the latest information on parr density.

### Increasing public awareness of F&W activities:

Increasing public awareness is not a specific goal of the study. However, journalists and the public are becoming increasingly aware of the importance of conserving biodiversity and genetic variability of Pacific salmon, and this study should lead to a better scientific (as well as public) understanding of how best to do that.

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## RELATIONSHIPS

### RELATED BPA PROJECT

8909800 Idaho supplementation studies (IDFG)

9102800 Monitoring the migrations of wild Snake River spring/summer chinook salmon smolts (NMFS)

9107300 Idaho natural production and evaluation, Intensive monitoring subproject (IDFG)

9005200 Performance/stock productivity impacts of hatchery supplementation (NBS)

9202601 Early life history study of Grande Ronde Basin chinook salmon (ODFW)

### RELATED NON-BPA PROJECT

### RELATIONSHIP

We coordinate genetic sampling with sampling from this study. We have provided genetic information for use in designing supplementation programs and studies.

We coordinate genetic sampling with sampling from this study. We also use their early-season snorkel surveys to help identify localities for sampling.

We coordinate genetic sampling with sampling from this study. We have provided genetic information for use in designing supplementation programs and studies.

In some years we have shared steelhead samples from this study. We provide NBS results of genetic analyses for some of their study streams.

We coordinate genetic sampling with sampling from this study.

### RELATIONSHIP

Smolt migration characteristics and parr-to-smolt survival of naturally produced spring chinook salmon in the Grande Ronde and Imnaha River Basins (part of Fish Passage Center smolt monitoring program)

Evaluation of reestablishing natural production of spring chinook salmon in Lookingglass Creek, Oregon, using a non-endemic hatchery stock (CTUIR and ODFW, funded through LSRCP) and Evaluation of the Lower Snake River Compensation Plan in Oregon (ODFW, funded through LSRCP).

We coordinate genetic sampling with sampling from this study

We have analyzed samples from Lookingglass Creek collected as part of this study, and we have provided considerable genetic information for evaluating the Lower Snake River Compensation Plan in Oregon

#### OPPORTUNITIES FOR COOPERATION:

We expect to continue our cooperation with the projects listed above in the future. In addition, for the past several years we have shared juvenile chinook salmon collected under our study with Drs. Diane Elliott and Ron Pascho of the National Biological Service, who use the samples for analysis of bacterial kidney disease in their study, "Juvenile fish transportation: Impact of bacterial kidney disease on survival of spring/summer chinook salmon stocks," funded by the U.S. Army Corps of Engineers (COE). This collaboration has been temporarily suspended because only fin clips were collected in 1995 and 1996 but may resume in 1997 if parr abundance warrants it.

#### COSTS AND FTE

1997 Planned: \$250,000

#### FUTURE FUNDING NEEDS:

<u>FY</u>	<u>\$ NEED</u>	<u>% PLAN</u>	<u>% IMPLEMENT</u>	<u>% O AND M</u>
1998	\$250,000		100%	
1999	\$250,000		100%	
2000	\$250,000		100%	
2001	\$250,000		100%	
2002	\$250,000		100%	

#### PAST OBLIGATIONS (incl. 1997 if done):

<u>FY</u>	<u>OBLIGATED</u>
1989	\$213,300
1991	\$433,800
1992	\$299,800
1993	\$260,000
1994	\$248,000
1995	\$250,700
1996	\$230,800

TOTAL: \$1,936,400

Note: Data are past obligations, or amounts committed by year, not amounts billed. Does not include data for related projects.

<u>FY</u>	<u>OTHER FUNDING SOURCE</u>	<u>AMOUNT</u>	<u>IN-KIND VALUE</u>
1998	ODFW, IDFG, WDFW, USFWS, CTUIR	\$10,000	
1999	ODFW, IDFG, WDFW, USFWS, CTUIR	\$10,000	
2000	ODFW, IDFG, WDFW, USFWS, CTUIR	\$10,000	
2001	ODFW, IDFG, WDFW, USFWS, CTUIR	\$10,000	
2002	ODFW, IDFG, WDFW, USFWS, CTUIR	\$10,000	

#### OTHER NON-FINANCIAL SUPPORTERS:

N/A

**LONGER TERM COSTS:** If monitoring continues beyond 2002, costs would be approximately \$250,000 per year.  
Continued implementation

**1997 OVERHEAD PERCENT:** 45.6% of total direct labor charges

**HOW DOES PERCENTAGE APPLY TO DIRECT COSTS:**

45.6% of total direct labor charges

**CONTRACTOR FTE:** 1 FTE

**SUBCONTRACTOR FTE:** 0 - 0.1

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